In Table 2, page 40 please add the following:

--Seq. 8-13: artificial sequence primers

Seq. 14: Pea albumin, nucleotide sequence

Seq. 15: Pea albumin, protein sequence

Seq. 16: sulfur-rich 15KD maize protein, nucleotide sequence

Seq. 17: sulfur-rich 15KD maize protein, protein sequence

Seq. 18: methionine-rich 10KD maize protein, nucleotide sequence

Seq. 19: methionine-rich 10 KD maize protein, protein sequence

Seq. 20: sulfur-rich rice prolamine, nucleotide sequence

Seq. 21: sulfur-rich rice prolamine, protein sequence

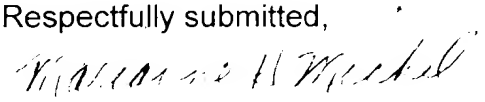
Seq. 22: wheat endosperm purothionin, protein sequence --

REMARKS

It is believed that the above amendments bring the application in compliance with 37 CFR 1.821-1.825.

In view of the above amendments, reconsideration and allowance of the above-identified application is respectfully requested.

Respectfully submitted,



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AMENDMENT WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown as a strike through, and inserted material is shown as underlined.

Page 28 is amended as follows:

designed based upon the published alpha hordothionin sequence to amplify the gene and to introduce a NcoI site at the start (ATG) codon and a BamHI site after the stop codon of the thionin coding sequence to facilitate cloning.

Primers are designated as HTPCR1 Seq. 8 (5'-AGTATAAGTAAACACACCATCACACCCTTGAGGCCCTTGCTGGTGGCCATGGT G-3') and HTPCR2 Seq. 9 (5'-CCTCACATCCCTTAGTGCCTAAGTTCGACGTCGGGCCCTCTAGTCGACGGATC CA-3'). These primers are used in a PCR reaction to amplify alpha hordothionin by conventional methods. The resulting PCR product is purified and subcloned into the BamHI/NcoI digested pBSKP vector (Stratagene, LaJolla, CA) and sequenced on both strands to confirm its identity. The clone is designated pBSKP-HT (seq. ID 1). Primers are designed for single stranded DNA site-directed mutagenesis to introduce 12 codons for lysine, based on the peptide structure of hordothionin 12 (Ref: Rao *et al.* 1994 Protein Engineering 7(12):1485-1493) and are designated HT12mut1 Seq. 10 (5'-AGCGGAAAATGCCCGAAAGGCTTCCCCAAATTGGC-3'), HT12mut2 Seq. 11 (5'-TGCGCAGGCGTCTGCAAGTGTAAGCTGACTAGTAGCGGAAAATGC-3'), HT12mut3 Seq. 12 (5'-TACAACCTTTGCAAAGTCAAAGGCGCCAAGAAGCTTTGCGCAGGCGTCTG-3'),

HT12mut4 Seq. 13 (5'-GCAAGAGTTGCTGCAAGAGTACCCTGGGAAGGAAGTGCTACAACCTTTGC-3').

Sequence analysis is used to verify the desired sequence of the resulting plasmid, designated pBSKP-HT12 (seq. ID 2).

Table 2: SEQUENCE INFORMATION

SEQUENCE ID	PROMOTER	GENE
Seq. 1: pBSKP-HT	None	3361-2947
Seq. 2: pBSKP-HT12	None	3361-2947
Seq. 3: PHP8001gz::HT12::gz expression vector	676-2198	2199-2612
Seq. 4: PHP7999 glb1::HT12::glb1 expression vector	3271-1834	1834-1420
Seq. 5: PHP5025 wx::HT::wx expression vector	43-1342	1343-1757
Seq. 6: PHP 11260 gz::ESA::gz expression vector	676-2198	2199-2675
Seq. 7: PHP11427 gz::BHL::gz	676-2198	2199-2450

Seq. 8-13: artificial sequence primers

Seq. 14: Pea albumin, nucleotide sequence

Seq. 15: Pea albumin, protein sequence

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Seq. 20: sulfur-rich rice prolamine, nucleotide sequence

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